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Sequence Listing was accepted.

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Reviewer: Durreshwar Anjum

Timestamp: [year=2009; month=6; day=24; hr=15; min=9; sec=56; ms=141;]

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Application No: 10585964 Version No: 2.0

Input Set:**Output Set:**

Started: 2009-06-17 11:38:51.859
Finished: 2009-06-17 11:38:54.570
Elapsed: 0 hr(s) 0 min(s) 2 sec(s) 711 ms
Total Warnings: 22
Total Errors: 0
No. of SeqIDs Defined: 23
Actual SeqID Count: 23

Error code	Error Description
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W 213	Artificial or Unknown found in <213> in SEQ ID (18)
W 213	Artificial or Unknown found in <213> in SEQ ID (19)
W 213	Artificial or Unknown found in <213> in SEQ ID (20)
W 213	Artificial or Unknown found in <213> in SEQ ID (21)

Input Set:

Output Set:

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Total Warnings: 22
Total Errors: 0
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Actual SeqID Count: 23

Error code

Error Description

This error has occurred more than 20 times, will not be displayed

SEQUENCE LISTING

<110> New England Biolabs, Inc.
Guan, Chudi
Kumar, Sanjay
Kucera, Rebecca

<120> Modified DNA Cleavage Enzymes and Methods of Use (as amended by
ISA)

<130> NEB-236-PUS

<140> 10585964

<141> 2006-07-13

<150> 60/524,123

<151> 2003-11-21

<150> PCT/US04/039288

<151> 2004-11-22

<160> 23

<170> PatentIn version 3.5

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gtgccttatg taattccggc gagcaatcac acttacactc cagacttctt acttccaaac	180
ggtatatctg ttgagacaaa ggggtctgtgg gaaagcgatg atagaaagaa gcacttatta	240
attagggagc agcaccgccg gctagacatc cgtattgtct tctcaagctc acgtactaag	300
ttatacaaaag gttctccaac gtcttatgga gagttctgcg aaaagcatgg tattaagttc	360
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<221> misc_feature

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<220>

<223> enterobacteria phage T7

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Ser Gly Leu Glu Asp Lys Val Ser Lys Gln Leu Glu Ser Lys Gly Ile
20 25 30

Lys Phe Glu Tyr Glu Glu Trp Lys Val Pro Tyr Val Ile Pro Ala Ser
35 40 45

Asn His Thr Tyr Thr Pro Asp Phe Leu Leu Pro Asn Gly Ile Phe Val
50 55 60

Glu Thr Lys Gly Leu Trp Glu Ser Asp Asp Arg Lys Lys His Leu Leu
65 70 75 80

Ile Arg Glu Gln His Pro Glu Leu Asp Ile Arg Ile Val Phe Ser Ser
85 90 95

Ser Arg Thr Lys Leu Tyr Lys Gly Ser Pro Thr Ser Tyr Gly Glu Phe
100 105 110

Cys Glu Lys His Gly Ile Lys Phe Ala Asp Lys Leu Ile Pro Ala Glu
115 120 125

Trp Ile Lys Glu Pro Lys Lys Glu Val Pro Phe Asp Arg Leu Lys Arg
130 135 140

Lys Gly Gly Lys Lys
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<210> 13

<211> 151

<212> PRT

<213> unknown

<220>

<223> yersinia pestis phage phiA1122

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Met Ala Gly Thr Tyr Ala Ala Arg Gly Ile Arg Lys Val Gly Thr Phe
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Arg Ser Gly Leu Glu Asp Lys Val Ser Lys Gln Leu Glu Gly Lys Gly
20 25 30

Ile Lys Phe Asp Tyr Glu Leu Trp Lys Ile Pro Tyr Val Val Pro Ala
35 40 45

Ser Asn His Val Tyr Thr Pro Asp Phe Leu Leu Pro Asn Gly Ile Phe
50 55 60

Ile Glu Thr Lys Gly Leu Trp Glu Ser Asp Asp Arg Lys Lys His Leu
65 70 75 80

Leu Ile Arg Glu Gln Phe Pro Glu Leu Asp Ile Arg Leu Val Phe Ser
85 90 95

Ser Ser Arg Thr Lys Leu Tyr Lys Gly Ser Pro Thr Ser Tyr Gly Glu
100 105 110

Trp Cys Glu Lys His Gly Ile Leu Phe Ala Asp Lys Leu Ile Pro Val
115 120 125

Glu Trp Leu Lys Glu Pro Lys Lys Glu Val Pro Phe Asp Arg Leu Lys
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Gln Ala Lys Gly Gly Lys Lys
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<210> 14

<211> 153

<212> PRT

<213> unknown

<220>

<223> bacteriophage phiYe03-12

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20 25 30

Ile Lys Phe Asp Tyr Glu Leu Trp Arg Ile Pro Tyr Val Ile Pro Ala
35 40 45

Ser Asp His Leu Tyr Thr Pro Asp Phe Leu Leu Pro Asn Gly Ile Phe
50 55 60

Ile Glu Thr Lys Gly Leu Trp Asp Ser Asp Asp Arg Lys Lys His Leu
65 70 75 80

Leu Ile Arg Glu Gln His Pro Glu Leu Asp Ile Arg Leu Val Phe Ser
85 90 95

Ser Ser Arg Ser Lys Leu Tyr Lys Gly Ser Pro Thr Ser Tyr Ala Glu
100 105 110

Trp Cys Glu Lys His Gly Ile Leu Phe Ala Asp Lys Leu Ile Pro Val
115 120 125

Glu Trp Leu Lys Glu Pro Lys Lys Glu Val Pro Phe Asp Lys Phe Lys
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Thr Lys Lys Gly Val Lys Lys Asn Gly
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<210> 15

<211> 152

<212> PRT

<213> Bacteriophage T3

<400> 15

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Ser Gly Leu Glu Asp Lys Val Ser Lys Gln Leu Glu Ser Lys Gly Ile
20 25 30

Lys Phe Asp Tyr Glu Leu Trp Arg Ile Pro Tyr Val Ile Pro Glu Ser
35 40 45

Asp His Leu Tyr Thr Pro Asp Phe Leu Leu Pro Asn Gly Ile Phe Ile
50 55 60

Glu Thr Lys Gly Leu Trp Asp Ser Asp Asp Arg Lys Lys His Leu Leu
65 70 75 80

Ile Arg Glu Gln His Pro Glu Leu Asp Ile Arg Leu Val Phe Ser Ser
85 90 95

Ser Arg Ser Lys Leu Tyr Lys Gly Ser Pro Thr Ser Tyr Gly Glu Trp
100 105 110

Cys Glu Lys His Gly Ile Leu Phe Ala Asp Lys Leu Ile Pro Val Ala
115 120 125

Gly Val Lys Glu Pro Lys Lys Glu Val Pro Phe Asp Lys Phe Lys Thr
130 135 140

Lys Lys Gly Val Lys Lys Asn Gly
145 150

<210> 16

<211> 147

<212> PRT

<213> unknown

<220>

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<400> 16

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Gly Leu Glu Asp Arg Asn Ala Lys His Met Asp Lys Leu Gly Val Lys
20 25 30

Tyr Asp Phe Glu Arg Phe His Ile Asn Tyr Val Val Pro Ala Arg Asp

35

40

45

Ala Lys Tyr Thr Pro Asp Phe Val Leu Ala Asn Gly Ile Ile Ile Glu
 50 55 60

Thr Lys Gly Ile Trp Glu Val Asp Asp Arg Lys Lys His Leu Leu Ile
 65 70 75 80

Arg Glu Gln Tyr Pro Asp Leu Asp Ile Arg Leu Val Phe Ser Asn Ser
 85 90 95

Asn Ser Lys Ile Tyr Lys Gly Ser Pro Thr Ser Tyr Ala Asp Phe Cys
 100 105 110

Thr Lys His Gly Ile Gln Phe Ala Asp Lys Leu Val Pro Arg Asp Trp
 115 120 125

Leu Lys Glu Ala Arg Lys Glu Ile Pro Gln Gly Val Leu Val Pro Lys
 130 135 140

Lys Gly Gly
 145

<210> 17

<211> 141

<212> PRT

<213> unknown

<220>

<223> pseudomonas putida KT2440

<400> 17

Met Gly Leu Lys Tyr Gly Phe Arg Ser Gly Leu Glu Glu Arg Ala Ala
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Asp Gln Leu Thr Ala Val Gly Met Gly Phe Thr Phe Glu Ser Leu Val
 20 25 30

Val Pro Tyr Thr Arg Pro Ala Lys Val His Lys Tyr Thr Pro Asp Phe
 35 40 45

Ala Leu Ala Asn Gly Ile Ile Val Glu Thr Lys Gly Arg Phe Leu Thr
 50 55 60

Glu Asp Arg Gln Lys Gln Leu Leu Val Lys Ala Gln His Pro Glu Leu
65 70 75 80

Asp Val Arg Phe Val Phe Ser Asn Ser Lys Thr Lys Ile Asn Lys Arg
85 90 95

Ser Thr Thr Thr Tyr Ala Asp Trp Cys Ser Lys Asn Gly Phe Gln Tyr
100 105 110

Ala Asp Lys Leu Val Pro His Ala Trp Leu Asn Glu Pro Val Asn Glu
115 120 125

Ala Ser Leu Ser Ile Ile Lys Gly Leu Ser Lys Glu Lys
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<210> 18

<211> 134

<212> PRT

<213> unknown

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<223> roseophage SI01

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Tyr Arg Ser Gly Leu Glu Glu Gln Thr Ala Lys Asp Leu Lys Lys Arg
20 25 30

Lys Val Leu Phe Thr Tyr Glu Glu Thr Lys Ile Lys Trp Leu Asp Ser
35 40 45

Lys Val Arg Thr Tyr Thr Pro Asp Phe Val Leu Pro Asn Gly Val Ile
50 55 60

Ile Glu Thr Lys Gly Arg Phe Val Ala Ala Asp Arg Arg Lys His Leu
65 70 75 80

Glu Ile Gln Lys Gln Phe Gly Thr Leu Tyr Asp Ile Arg Phe Val Phe
85 90 95

Thr Asn Ser Lys Ala Lys Leu Tyr Lys Gly Ala Lys Ser Ser Tyr Ala
100 105 110

Asp Trp Cys Asn Lys His Gly Phe Leu Tyr Ala Asp Lys Thr Ile Pro
115 120 125

Glu Asp Trp Leu Asn Glu
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<210> 19

<211> 14

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<220>

<221> misc_feature

<222> (9)..(9)

<223> mismatch

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<222> (15)..(15)

<223> mismatch

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<210> 21

<211> 18

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<213> unknown

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<400> 21
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<210> 22
<211> 149
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<220>
<223> enterobacteria phage T7

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Met Ala Gly Tyr Ser Ala Lys Gly Ile Arg Lys Val Gly Ala Phe Arg
1 5 10 15

Ser Gly Leu Glu Asp Lys Val Ser Lys Gln Leu Glu Ser Lys Gly Ile
20 25 30

Lys Phe Glu Tyr Glu Glu Trp Lys Val Pro Tyr Val Ile Pro Ala Ser
35 40 45

Asn His Thr Tyr Thr Pro Asp Phe Leu Leu Pro Asn Gly Ile Phe Val
50 55 60

Glu Thr Lys Gly Leu Trp Glu Ser Asp Asp Arg Lys Lys His Leu Leu
65 70 75 80

Ile Arg Lys Gln His Pro Glu Leu Asp Ile Arg Ile Val Phe Ser Ser
85 90 95

Ser Arg Thr Lys Leu Tyr Lys Gly Ser Pro Thr Ser Tyr Gly Glu Phe
100 105 110

Cys Glu Lys His Gly Ile Lys Phe Ala Asp Lys Leu Ile Pro Ala Glu
115 120 125

Trp Ile Lys Glu Pro Lys Lys Glu Val Pro Phe Asp Arg Leu Lys Arg
130 135 140

Lys Gly Gly Lys Lys
145

<210> 23

<211> 149

<212> PRT

<213> unknown

<220>

<223> enterobacteria phage T7

<400> 23

Met Val Gly Tyr Gly Val Lys Gly Ile Arg Lys Val Gly Ala Phe Arg
1 5 10 15

Ser Gly Leu Glu Asp Lys Val Ser Lys Gln Leu Glu Ser Lys Gly Ile
20 25 30

Lys Phe Glu Tyr Glu Glu Trp Lys Val Pro Tyr Val Ile Pro Ala Ser
35 40 45

Asn His Thr Tyr Thr Pro Asp Phe Leu Leu Pro Asn Gly Ile Phe Val
50 55 60

Glu Thr Lys Gly Leu Trp Glu Ser Asp Asp Arg Lys Lys His Leu Leu
65 70 75 80

Ile Arg Glu Gln His Pro Glu Leu Asp Ile Arg Ile Val Phe Ser Ser
85 90 95

Ser Arg Thr Lys Leu Tyr Lys Gly Ser Pro Thr Ser Tyr Gly Glu Phe
100 105 110

Cys Glu Lys His Gly Ile Lys Phe Ala Asp Lys Leu Ile Pro Ala Glu
115 120 125

Trp Ile Lys Glu Pro Lys Lys Glu Val Ser Phe Asp Arg Leu Lys Arg
130 135 140

Lys Gly Gly Lys Lys
145

